

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: TANZI, RUDOLPH
WASCO, WILMA

(ii) TITLE OF INVENTION: Genetic Alterations Related To Familial
Alzheimer's Disease

(iii) NUMBER OF SEQUENCES: 32

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
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(C) CITY: WASHINGTON
(D) STATE: DC
(E) COUNTRY: USA
(F) ZIP: 20005-3934

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To be assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/706,344
(B) FILING DATE: 30-AUG-1996

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/003,054
(B) FILING DATE: 31-AUG-1995

(ix) ATTORNEY/AGENT INFORMATION:

(A) NAME: KIM, JUDITH U.
(B) REGISTRATION NUMBER: 40,679
(C) REFERENCE/DOCKET NUMBER: 0609.4180002

(x) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 202-371-2600
(B) TELEFAX: 202-371-2540

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2765 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 249..1649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TGGGACAGGC AGCTCCGGGG TCCGCGGTTT CACATCGGAA	ACAAAACAGC GGCTGGTCTG	60
GAAGGAAACCT GAGCTACGAG CGCGGGCGGC AGCGGGGGCGG	CGGGAAAGCG TATACTTAAT	120
CTGGGAGCCT GCAAGTGACA ACAGCCTTTG CGGTCTTAG ACAGCTTGGC	CTGGAGGAGA	180
ACACATGAAA GAAAAGAACCT CAAGAGGCTT TGTTTCTGT	GAAACAGTAT TTCTATACAG	240
TTGCTCCA ATG ACA GAG TTA CCT GCA CCG TTG TCC	CAG AAT GCA	290
Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala	1 5 10	
CAG ATG TCT GAG GAC AAC CAC CTG AGC AAT ACT	GTA CGT AGC CAG AAT	338
Gln Met Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn	15 20 25 30	
GAC AAT AGA GAA CGG CAG GAG CAC AAC GAC AGA CGG AGC CTT GGC CAC	386	
Asp Asn Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His	35 40 45	
CCT GAG CCA TTA TCT AAT GGA CGA CCC CAG GGT AAC TCC CGG CAG GTG	434	
Pro Glu Pro Leu Ser Asn Gly Arg Pro Glu Gly Asn Ser Arg Gln Val	50 55 60	
GTG GAG CAA GAT GAG GAA GAA GAT GAG GAG CTG ACA TTG AAA TAT GGC	482	
Val Glu Gln Asp Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly	65 70 75	
GCC AAG CAT GTG ATC ATG CTC TTT GTC CCT GTG ACT CTC TGC ATG GTG	530	
Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val	80 85 90	
GTG GTC GTG GCT ACC ATT AAG TCA GTC AGC TTT TAT ACC CGG AAG GAT	578	
Val Val Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp	95 100 105 110	
GGG CAG CTA ATC TAT ACC CCA TTC ACA GAA GAT ACC GAG ACT GTG GGC	626	
Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly	115 120 125	
CAG AGA GCC CTG CAC TCA ATT CTG AAT GCT GCC ATC ATG ATC AGT GTC	674	
Gln Arg Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val	130 135 140	
ATT GTT GTC ATG ACT ATC CTC CTG GTG GTT CTG TAT AAA TAC AGG TGC	722	
Ile Val Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys	145 150 155	
TAT AAG GTC ATC CAT GCC TGG CTT ATT ATA TCA TCT CTA TTG TTG CTG	770	
Tyr Lys Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu	160 165 170	
TTC TTT TTT TCA TTC ATT TAC TTG GGG GAA GTG TTT AAA ACC TAT AAC	818	
Phe Phe Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn	175 180 185 190	
GTT GCT GTG GAC TAC ATT ACT GTT GCA CTC CTG ATC TGG AAT TTT GGT	866	
Val Ala Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly	195 200 205	

GTG GTG GGA ATG ATT TCC ATT CAC TGG AAA GGT CCA CTT CGA CTC CAG Val Val Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln 210 215 220	914
CAG GCA TAT CTC ATT ATG ATT AGT GCC CTC ATG GCC CTG GTG TTT ATC Gln Ala Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile 225 230 235	962
AAG TAC CTC CCT GAA TGG ACT GCG TGG CTC ATC TTG GCT GTG ATT TCA Lys Tyr Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser 240 245 250	1010
GTA TAT GAT TTA GTG GCT TTG TGT CCG AAA GGT CCA CTT CGT ATG Val Tyr Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met 255 260 265 270	1058
CTG GTT GAA ACA GCT CAG GAG AGA AAT GAA ACG CTT TTT CCA GCT CTC Leu Val Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu 275 280 285	1106
ATT TAC TCC TCA ACA ATG GTG TGG TTG GTG AAT ATG GCA GAA GGA GAC Ile Tyr Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp 290 295 300	1154
CCG GAA GCT CAA AGG AGA GTA TCC AAA AAT TCC AAG CAT AAT GCA GAA Pro Glu Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu 305 310 315	1202
AGC ACA GAA AGG GAG TCA CAA GAC ACT GTT GCA GAG AAT GAT GAT GGC Ser Thr Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly 320 325 330	1250
GGG TTC AGT GAG GAA TGG GAA GCC CAG AGG GAC AGT CAT CTA GGG CCT Gly Phe Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro 335 340 345 350	1298
CAT CGC TCT ACA CCT GAG TCA CGA GCT GTC CAG GAA CTT TCC AGC His Arg Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser 355 360 365	1346
AGT ATC CTC GCT GGT GAA GAC CCA GAG GAA AGG GGA GTA AAA CTT GGA Ser Ile Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly 370 375 380	1394
TTG GGA GAT TTC ATT TTC TAC AGT GTT CTG GTT GGT AAA GCC TCA GCA Leu Gly Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala 385 390 395	1442
ACA GCC ACT GGA GAC TGG AAC ACA ACC ATA GCC TGT TTC GTA GCC ATA Thr Ala Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile 400 405 410	1490
TTA ATT GGT TTG TGC CTT ACA TTA TTA CTC CTT GCC ATT TTC AAG AAA Leu Ile Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys 415 420 425 430	1538
GCA TTG CCA GCT CTT CCA ATC TCC ATC ACC TTT GGG CTT GTT TTC TAC Ala Leu Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr 435 440 445	1586
TTT GCC ACA GAT TAT CTT GTA CAG CCT TTT ATG GAC CAA TTA GCA TTC Phe Ala Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe	1634

	450	455	460	
CAT CAA TTT TAT ATC TAGCATATT GCGGTTAGAA TCCCCATGGAT GTTTCTTC				1689
His Gln Phe Tyr Ile				
465				
TGACTATAAC CAAATCTGGG GAGGACAAAG GTGATTTCC TGTGTCCACA TCTAACAAAG				1749
TCAGAGATTCC CGGCTGGACT TTTCAGCTT CCTTCCAAGT CTTCTGACC ACCTTGCACT				1809
ATTGGACTTT GGAAGGAGGT GCCTATAGAA AACGATTTG AACATACCTTC ATCGCAGTGG				1869
ACTGTGTCCC TCGGTGCAGA AACTACCAGA TTGAGGGAC GAGGTCAAGG AGATATGATA				1929
GGCCCGGAAG TTGCTGTGCC CCATCAGCAG CTTGACGCGT GGTCACAGGA CGATTTCACT				1989
GACACTGCGA ACTCTCAGGA CTACCGGTTA CCAAGAGGTT AGGTGAAAGTG GTTTAACCA				2049
AACGGAACCTT TCATCTTAA ACTACACGTT GAAAATCAAC CCAATAATT TGTTAAACT				2109
GAATTCTGAA CTTTCAGGA GGTACTGTGA GGAAGAGCAG GCACCAAGCAG CAGAATGGGG				2169
AATGGGAGG TGGGAGGGG TTCCAGCTT CCTTGATTT TTTGCTGCAG ACTCATCCTT				2229
TTTAAATGAG ACTTGTITTC CCCCTCTTT GAGTCAGTC AAATATGTAG ATTGCCTTTG				2289
GCAATTCTTC TTCTCAAGCA CTGACACTCA TTACCGCTCG TGATTGCCAT TTCTTCCAA				2349
GGCCAGCTCG AACCTGAGGT TGCTTTATCC TAAAAGTTT AACCTCAGGT TCCAAATTCA				2409
GTAAATTTG GAAACAGTAC AGCTATTTCT CATCAATTCT CTATCATGTT GAAGTCAAAT				2469
TTGGATTTT CACCAAATTCA TGAATTGTA GACATACTTG TACGCTCACT TGCCCCAGA				2529
TGCCTCCCTC GTCTCATTC TTCTCTCCA CACAAGCAGT CTTTTCTAC AGCCAGTAAG				2589
GCAGCTCTGT CRTGGTAGCA GATGGTCCCA TTATTCTAGG GTCTTACTCT TTGTATGATG				2649
AAAAGAATGT GTTATGAATC GGTGCTGTCA GCCCTGCTGT CAGACCTTCT TCCACAGCAA				2709
ATGAGATGTA TGCCCCAAAGC GGTAGAATTAA AGAAAGAGTA AAATGGCTGT TGAAGC				2765

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 467 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met	Thr	Glu	LLe	Pro	Ala	Pro	Leu	Ser	Tyr	Phe	Gln	Asn	Ala	Gln	Met
1							5				10				15

Ser	Glu	Asp	Asn	His	Leu	Ser	Asn	Thr	Val	Arg	Ser	Gln	Asn	Asp	Asn
								20				25			30

Arg	Glu	Arg	Gln	Glu	His	Asn	Asp	Arg	Arg	Ser	Leu	Gly	His	Pro	Glu
								35			40				45

Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu
50 55 60

Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
65 70 75 80

His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
85 90 95

Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
100 105 110

Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
115 120 125

Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
130 135 140

Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
145 150 155 160

Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Phe Phe
165 170 175

Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
180 185 190

Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val
195 200 205

Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
210 215 220

Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
225 230 235 240

Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
245 250 255

Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val
260 265 270

Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
275 280 285

Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
290 295 300

Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu Ser Thr
305 310 315 320

Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe
325 330 335

Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
340 345 350

Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile
355 360 365

Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
370 375 380

Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
385 390 395 400
Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
405 410 415
Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
420 425 430
Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
435 440 445
Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
450 455 460
Phe Tyr Ile
465

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2765 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 249..1649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TGGGACAGGC AGCTCCGGGG TCCGCGGTTT CACATCGGAA ACAAAACAGC GGCTGGTCTG 60
GAAGGAACCT GAGCTACGAG CGCGCGCGC AGCGGGGCGG CGGGGAAGCG TATACTTAAT 120
CTGGGAGCCT GCAAGTGTACA ACAGCCTTTG CGGTCTTAG ACAGCTTGCC CTGGAGGAGA 180
ACACATGAAA GAAAGAACCT CAAGAGGCTT TGTTTTCTGT GAAACAGTAT TTCTATACAG 240
TTGCTCCA ATG ACA GAG TTA CCT GCA CGG TTG TCC TAC TTC CAG AAT GCA 290
Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala
1 5 10
CAG ATG TCT GAG GAC AAC CAC CTG AGC AAT ACT GTA CGT AGC CAG AAT 338
Gln Met Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn
15 20 25 30
GAC AAT AGA GAA CGG CAG GAG CAC AAC GAC AGA CGG AGC CTT GGC CAC 386
Asp Asn Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His
35 40 45
CCT GAG CCA TTA TCT AAT GGA CGA CCC CAG GGT AAC TCC CGG CAG GTG 434
Pro Glu Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val
50 55 60
GTG GAG CAA GAT GAG GAA GAA GAT GAG GAG CTG ACA TTG AAA TAT GGC 482
Val Glu Gln Asp Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly

65	70	75	
GCC AAG CAT GTG ATC ATG CTC TTT GTC CCT GTG ACT CTC TGC ATG GTG Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val 80 85 90			530
GTG GTC GTG GCT ACC ATT AAG TCA GTC AGC TTT TAT ACC CGG AAG GAT Val Val Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp 95 100 105 110			578
GGG CAG CTA ATC TAT ACC CCA TTC ACA GAA GAT ACC GAG ACT GTG GGC Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly 115 120 125			626
CAG AGA GCC CTG CAC TCA ATT CTG AAT GCT GCC ATC ATG ATC AGT GTC Gln Arg Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val 130 135 140			674
ATT GTT GTC ATG ACT ATC CTC CTG GTG GTT CTG TAT AAA TAC AGG TGC Ile Val Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys 145 150 155			722
TAT AAG GTC ATC CAT GCC TGG CTT ATT ATA TCA TCT CTA TTG TTG CTG Tyr Lys Val Ile His Ala Trp Leu Ile Ser Ser Leu Leu Leu Leu 160 165 170			770
TTC TTT TTT TCA TTC ATT TAC TTG GGG GAA GTG TTT AAA ACC TAT AAC Phe Phe Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn 175 180 185 190			818
GTT GCT GTG GAC TAC ATT ACT GTT GCA CTC CTG ATC TGG AAT TTT GGT Val Ala Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly 195 200 205			866
GTG GTG GGA ATG ATT TCC ATT CAC TGG AAA GGT CCA CTT CGA CTC CAG Val Val Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln 210 215 220			914
CAG GCA TAT CTC ATT ATG ATT AGT GCC CTC ATG GCC CTG GTG TTT ATC Gln Ala Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile 225 230 235			962
AAG TAC CTC CCT GAA TGG ACT GCG TGG CTC ATC TTG GCT GTG ATT TCA Lys Tyr Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser 240 245 250			1010
GTA TAT GAT TTA GTG GCT GTT TTG CGT CTG AAA GGT CCA CTT CAT ATG Val Tyr Asp Leu Val Ala Val Leu Arg Leu Lys Gly Pro Leu His Met 255 260 265 270			1058
CTG GTT GAA ACA GCT CAG GAG AGA AAT GAA ACG CTT TTT CCA GCT CTC Leu Val Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu 275 280 285			1106
ATT TAC TCC TCA ACA ATG GTG TGG TTG GTG AAT ATG GCA GAA GGA GAC Ile Tyr Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp 290 295 300			1154
CCG GAA GCT CAA AGG AGA GTA TCC AAA AAT TCC AAG CAT AAT GCA GAA Pro Glu Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu 305 310 315			1202

AGC ACA GAA AGG GAG TCA CAA GAC ACT GTT GCA GAG AAT GAT GAT GGC Ser Thr Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly 320 325 330	1295
GGG TTC AGT GAG GAA TGG GAA GCC CAG AGG GAC AGT CAT CTA GGG CCT Gly Phe Ser Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro 335 340 345 350	1298
CAT CGC TCT ACA CCT GAG TCA CGA GCT GCT GTC CAG GAA CTT TCC AGC His Arg Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser 355 360 365	1346
AGT ATC CTC GCT GGT GAA GAC CCA GAG GAA AGG GGA GTA AAA CTT GGA Ser Ile Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly 370 375 380	1394
TTG GGA GAT TTC ATT TTC TAC AGT GTT CTG GTT GGT AAA GCC TCA GCA Leu Gly Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala 385 390 395	1442
ACA GCC AGT GGA GAC TGG AAC ACA ACC ATA GCC TGT TTC GTA GCC ATA Thr Ala Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile 400 405 410	1490
TTA ATT GGT TTG TGC CTT ACA TTA TTA CTC CTT GCC ATT TTC AAG AAA Leu Ile Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys 415 420 425 430	1538
GCA TTG CCA GCT CTT CCA ATC TCC ATC ACC TTT GGG CTT GTT TTC TAC Ala Leu Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr 435 440 445	1586
TTT GCC ACA GAT TAT CTT GTA CAG CCT TTT ATG GAC CAA TTA GCA TTC Phe Ala Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe 450 455 460	1634
CAT CAA TTT TAT ATC TAGCATATT GCGGTTAGAA TCCCCATGGAT GTTTCTTCTT His Gln Phe Tyr Ile 465	1689
TGACTATAAC CAAATCTGGG GAGGACAAAG GTGATTTCC TGTGTCCACA TCTAACAAAG TCAAGATTCC CGGGTGGACT TTTGCAGCTT CCTTCCAAGT CTTCTGACC ACCTTGCACT ATTGGACTTT GGAAGGGAGT GCCTATAGAA AACGATTTTG AACATACTTC ATGCCAGTGG ACTGTGTCCC TCGGTGCAGA AACTACCAGA TTTGAGGGAC GAGGTCAAGG AGATATGATA GGCCCGGAAG TTGCTGTGCC CCATCAGCG CTTGACGCCTT GGTACAGGA CGATTTCACT GACACTGCGA ACTCTCAGGA CTACCGGTTA CCAAGAGGTT AGGTGAAGTG GTTTAAACCA AACGGAACCTC TTCTATCTTAA ACTACACGTT GAAAATCAAC CCAATAATTG TGATTAACCT GAATTCTGAA CTTTCAGGA GGTACTGTGA GGAAGAGCAG GCACCAGCAG CAGAATGGGG AATGGAGAGG TGGGCAGGGG TTCCAGCTTC CCTTTGATTT TTTGCTGCAG ACTCATCCTT TTTAAATGAG ACTTGTTTC CCCTCTCTT GAGTCAAGTC AAATATGTAG ATTGCCTTG GCAATTCTTC TTCTCAAGCA CTGACACTCA TTACCGTCTG TGATTGCCAT TTCTTCCCAA	1749 1809 1869 1929 1989 2049 2109 2169 2229 2289 2349

GGCCAGTCTG AACCTGAGGT TGCTTTATCC TAAAAAGTTT AACCTCAGGT TCCAAATTCA	2409
GTAAATTTG GAAACAGTAC AGCTATTCT CATCAATTCT CTATCATGTT GAAAGTCAAAT	2469
TTGGATTTTC CACCAAATTG TGAAATTGTA GACATACTTG TAGGCTCACT TGCCCCCAGA	2529
TGCCTCCTCT GTCCTCATTC TTCTCTCCCA CACAAGCAGT CTTTTCTAC AGCCAGTAAG	2589
GCAGCTCTGT CRTGGTAGCA GATGGTCCCA TTATTCTAGG GTCTTACTCT TTGTATGATG	2649
AAAAGAATGT GTTATGAATC GGTGCTGTCA GCCCTGTGT CAGACCTTCT TCCACAGCAA	2709
ATGAGATGTA TGCCCAAAGC GGTAGAATTA AAGAAGAGTA AAATGGCTGT TGAAGC	2765

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met	
1 5 10 15	
Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn Asp Asn	
20 25 30	
Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His Pro Glu	
35 40 45	
Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu	
50 55 60	
Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys	
65 70 75 80	
His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val	
85 90 95	
Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln	
100 105 110	
Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg	
115 120 125	
Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val	
130 135 140	
Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys	
145 150 155 160	
Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Phe Phe	
165 170 175	
Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala	
180 185 190	
Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val	

195	200	205
Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala		
210	215	220
Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr		
225	230	235
240		
Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr		
245	250	255
Asp Leu Val Ala Val Leu Arg Leu Lys Gly Pro Leu His Met Leu Val		
260	265	270
Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr		
275	280	285
Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu		
290	295	300
Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu Ser Thr		
305	310	315
320		
Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe		
325	330	335
Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg		
340	345	350
Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile		
355	360	365
Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly		
370	375	380
Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala		
385	390	395
400		
Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile		
405	410	415
Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu		
420	425	430
Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala		
435	440	445
Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln		
450	455	460
Phe Tyr Ile		
465		

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CACCCATTAA CAAGTTTAGC

20

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GATGAGACAA GTGCCGTGAA

20

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Gln Ala Ala Pro Gly Ser Ala Val Ser His Arg Lys Gln Asn Ser
1 5 10 15

Gly Trp Ser Gly Arg Asn Leu Ser Tyr Glu Pro Arg Arg Gln Arg Gly
20 25 30

Gly Gly Glu Ala Tyr Thr
35

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Gly Ser Leu Gln Val Thr Thr Ala Phe Ala Val Leu Arg Gln Leu
1 5 10 15

Gly Leu Glu Glu Asn Thr
20

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Lys Lys Glu Pro Gln Glu Ala Leu Phe Ser Val Lys Gln Tyr Phe Tyr
1 5 10 15

Thr Val Ala Pro
20

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

His Ile Cys Gly
1

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Asn Pro Met Asp Val Ser Ser Leu Thr Ile Thr Lys Ser Gly Glu Asp
1 5 10 15

Lys Gly Asp Phe Pro Val Ser Thr Ser Asn Lys Val Lys Ile Pro Gly
20 25 30

Trp Thr Phe Ala Ala Ser Phe Gin Val Phe Leu Thr Thr Leu His Tyr
35 40 45

Trp Thr Leu Glu Gly Ala Tyr Arg Lys Arg Phe
50 55 60

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Thr Tyr Phe Ile Ala Val Asp Cys Val Pro Arg Cys Arg Asn Tyr Gln
1 5 10 15

Ile

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gly Thr Arg Ser Arg Arg Tyr Asp Arg Pro Gly Ser Cys Cys Ala Pro
1 5 10 15

Ser Ala Ala

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Arg Val Val Thr Gly Arg Phe His
1 5

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

His Cys Glu Leu Ser Gly Leu Pro Val Thr Lys Arg Leu Gly Glu Val
1 5 10 15
Val

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Thr Lys Arg Asn Ser Ser Ser
1 5

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys Ser Thr Gln
1

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Phe Cys Ile Asn
1

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ile Leu Asn Phe Ser Gly Gly Thr Val Arg Lys Ser Arg His Gln Gln
1 5 10 15

Gln Asn Gly Glu Trp Arg Gly Gly Gln Gly Phe Gln Leu Pro Phe Asp
20 25 30

Phe Leu Leu Gln Thr His Pro Phe
35 40

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Arg Leu Val Phe Pro Ser Leu
1 5

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Val Lys Ser Asn Met
1 5

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ile Ala Phe Gly Asn Ser Ser Ser Gln Ala Leu Thr Leu Ile Thr Val
1 5 10 15
Cys Asp Cys His Phe Pro Arg Pro Val
20 25

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Gly Cys Phe Ile Leu Lys Val Leu Thr Ser Gly Ser Lys Phe Ser Lys
1 5 10 15
Phe Trp Lys Gln Tyr Ser Tyr Phe Ser Ser Ile Leu Tyr His Val Glu
20 25 30
Val Lys Phe Gly Phe Ser Thr Lys Phe
35 40

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ile	Cys	Arg	His	Thr	Cys	Thr	Leu	Thr	Cys	Pro	Gln	Met	Pro	Pro	Leu
1					5				10					15	
Ser	Ser	Phe	Phe	Ser	Pro	Thr	Gln	Ala	Val	Phe	Phe	Tyr	Ser	Gln	
					20				25				30		

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Gly	Ser	Ser	Val	Xaa	Val	Ala	Asp	Gly	Pro	Ile	Ile	Leu	Gly	Ser	Tyr
1					5				10				15		
Ser	Leu	Tyr	Asp	Glu	Lys	Asn	Val	Leu							
					20			25							

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Ile	Gly	Ala	Val	Ser	Pro	Ala	Val	Arg	Pro	Ser	Ser	Thr	Ala	Asn	Glu
1					5				10				15		
Met	Tyr	Ala	Gln	Ser	Gly	Arg	Ile	Lys	Glu	Glu					
					20			25							

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2765 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 249..1649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

TGGGACAGGC AGCTCCGGGG TCCCGGGTTT CACATCGGAA ACAAAACAGC GGCTGGTCTG	60
GAAGGAAACCT GAGCTACGAG CCGCGGCCGC AGCGGGGCCGG CGGGGAAGCG TATACCTAAT	120
CTGGGGACCT GCAAGTGACA ACAGCCTTTG CGGTCCCTTAG ACAGCTTGGC CTGGAGGAGA	180
ACACATGAAA GAAAGAACCT CAAGAGGCTT TGTTTTCTGT GAAACAGTAT TTCTATACAG	240
TTGCTCCA ATG ACA GAG TTA CCT GCA CCG TTG TCC TAC TTC CAG AAT GCA	290
Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala	
1 5 10	
CAG ATG TCT GAG GAC AAC CAC CTG AGC AAT ACT GTA CGT AGC CAG AAT	338
Gln Met Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn	
15 20 25 30	
GAC AAT AGA GAA CGG CAG GAG CAC AAC GAC AGA CGG AGC CTT GGC CAC	386
Asp Asn Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His	
35 40 45	
CCT GAG CCA TTA TCT AAT GGA CGA CCC CAG GGT AAC TCC CGG CAG GTG	434
Pro Glu Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val	
50 55 60	
GTG GAG CAA GAT GAG GAA GAA GAT GAG GAG CTG ACA TTG AAA TAT GGC	482
Val Glu Gln Asp Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly	
65 70 75	
GCC AAG CAT GTG ATC ATG CTC TTT GTC CCT GTG ACT CTC TGC ATG GTG	530
Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val	
80 85 90	
GTG GTC GTG GCT ACC ATT AAG TCA GTC AGC TTT TAT ACC CGG AAG GAT	578
Val Val Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp	
95 100 105 110	
GGG CAG CTA ATC TAT ACC CCA TTC ACA GAA GAT ACC GAG ACT GTG GGC	626
Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly	
115 120 125	
CAG AGA GCC CTG GAC TCA ATT CTG AAT GCT GCC ATC ATG ATC AGT GTC	674
Gln Arg Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val	
130 135 140	
ATT GTT GTC ATG ACT ATC CTC CTG GTG TTG CTG TAT AAA TAC AGG TGC	722

Ile Val Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys 145 150 155	
TAT AAG GTC ATC CAT GCC TGG CTT ATT ATA TCA TCT CTA TTG TTG CTG Tyr Lys Val Ile His Ala Trp Leu Ile Ser Ser Leu Leu Leu Leu 160 165 170	770
TTC TTT TTT TCA TTC ATT TAC TTG GGG GAA GTG TTT AAA ACC TAT AAC Phe Phe Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn 175 180 185 190	818
GTT GCT GTG GAC TAC ATT ACT GTT GCA CTC CTG ATC TGG AAT TTT GGT Val Ala Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly 195 200 205	866
GTG GTG GGA ATG ATT TCC ATT CAC TGG AAA GGT CCA CTT CGA CTC CAG Val Val Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln 210 215 220	914
CAG GCA TAT CTC ATT ATG ATT AGT GCC CTC ATG GCC CTG GTG TTT ATC Gln Ala Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile 225 230 235	962
AAG TAC CTC CCT GAA TGG ACT GCG TGG CTC ATC TTG GCT GTG ATT TCA Lys Tyr Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser 240 245 250	1010
GTA TAT GAT TTA GTG GCT GTT TTG CGT CCG AAA GGT CCA CTT CGT ATG Val Tyr Asp Leu Val Ala Val Leu Arg Pro Lys Gly Pro Leu Arg Met 255 260 265 270	1058
CTG GTT GAA ACA GCT CAG GAG AGA AAT GAA ACG CTT TTT CCA GCT CTC Leu Val Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu 275 280 285	1106
ATT TAC TCC TCA ACA ATG GTG TGG TTG GTG AAT ATG GCA GAA GGA GAC Ile Tyr Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp 290 295 300	1154
CCG GAA GCT CAA AGG AGA GTA TCC AAA AAT TCC AAG CAT AAT GCA GAA Pro Glu Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu 305 310 315	1202
AGC ACA GAA AGG GAG TCA CAA GAC ACT GTT GCA GAG AAT GAT GAT GGC Ser Thr Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly 320 325 330	1250
GGG TTC AGT GAG GAA TGG GAA GCC CAG AGG GAC AGT CAT CTA GGG CCT Gly Phe Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro 335 340 345 350	1298
CAT CGC TCT ACA CCT GAG TCA CGA GCT GCT GTC CAG GAA CTT TCC AGC His Arg Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser 355 360 365	1346
AGT ATC CTC GCT GGT GAA GAC CCA GAG GAA AGG GGA GTA AAA CTT GGA Ser Ile Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly 370 375 380	1394
TTG GGA GAT TTC ATT TTC TAC AGT GTT CTG GTT GGT AAA GCC TCA GCA Leu Gly Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala 385 390 395	1442

ACA GCC AGT GGA GAC TGG AAC ACA ACC ATA GCC TGT TTC GTA GCC ATA Thr Ala Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile 400	405	410	1490
TTA ATT GGT TTG TGC CTT ACA TTA TTA CTC CTT GCC ATT TTC AAG AAA Leu Ile Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys 415	420	425	430
GCA TTG CCA GCT CTT CCA ATC TCC ATC ACC TTT GGG CTT GTT TTC TAC Ala Leu Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr 435	440	445	1586
TTT GCC ACA GAT TAT CTT GTA CAG CCT TTT ATG GAC CAA TTA GCA TTC Phe Ala Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe 450	455	460	1634
CAT CAA TTT TAT ATC TAGCATATT TCGGGTTAGAA TCCCCATGGAT GTTTCTTCTT His Gln Phe Tyr Ile 465			1689
TGACTATAAC CAAATCTGGG GAGGACAAAG GTGATTTCC TGTGTCCACA TCTAACAAAG			1749
TCAAGATTCC CGGCTGGACT TTTGAGCTT CCTTCCAAGT CCTCCTGACC ACCTTGCACT			1809
ATTGGACTT GGAAGGAGGT GCCTATAGAA AACGATTTG AACATACCTTC ATGGCAGTGG			1869
ACTGTGTCCC TCGGTGCAGA AACTACCAGA TTTGAGGGAC GAGGTCAAGG AGATATGATA			1929
GGCCCGGAAG TTGCTGTGCC CCATCAGCG CTTGACCGGT GGTCACAGGA CGATTTCACT			1989
GACACTGCAGA ACTCTCAGGA CTACCGTTA CCAAGAGGTT AGGTGAAGTG GTTAAACCA			2049
AACGGAACCTC TTCATCTTAA ACTCACAGTT GAAAATCAAC CCAATAATT TGTTAAACT			2109
GAATTCTGAA CTTTCAGGA GGTACTGTGA GGAAGAGCAG GCACCAGCAG CAGAATGGGG			2169
AATGGGAGGG TGGGCAGGGG TTCCAGCTTC CCTTGATT TTTGCTGCAG ACTCATCCTT			2229
TTTAATGAG ACTTGTTC CCCTCTCTT GAGTCAGTC AAATATGAG ATTGCCTTG			2289
GCAATTCTTC TTCTCAAGCA CTGACACTCA TTACCGCTCTG TGATTGCCAT TTCTTCCCAA			2349
GGCCAGTCTG AACCTGAGGT TGCTTATCC TAAAAGTTT AACCTCAGGT TCCAAATTCA			2409
GTAAATTTG GAAACAGTAC AGCTATTCT CATCAATTCT CTATCATGTT GAAGTCAAAT			2469
TTGGATTTTC CACCAAATTG TGAATTGTA GACATACTTG TACGCTCACT TGCCCCCAGA			2529
TGCCTCTCT GTCCTCATTC TTCTCTCCCA CACAAGCAGT CTTTTCTAC AGCCAGTAAG			2589
GCAGCTCTGT CRTGGTAGCA GATGGTCCCA TTATTCTAGG GTCTTACTCT TTGTATGATG			2649
AAAAGAATGT GTTATGAATC GGTGCTGTCA GCCCTGCTGT CAGACCTCT TCCACAGCAA			2709
ATGAGATGTA TGCCCAAAGC GGTAGAATTAA AAGAAGAGTA AAATGGCTGT TGAAGC			2765

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 467 amino acids
(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met
1 5 10 15

Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn Asp Asn
20 25 30

Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His Pro Glu
35 40 45

Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu
50 55 60

Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
65 70 75 80

His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
85 90 95

Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
100 105 110

Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
115 120 125

Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
130 135 140

Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
145 150 155 160

Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Phe Phe
165 170 175

Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
180 185 190

Val Asp Tyr Ile Thr Val Ala Leu Ile Trp Asn Phe Gly Val Val
195 200 205

Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
210 215 220

Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
225 230 235 240

Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
245 250 255

Asp Leu Val Ala Val Leu Arg Pro Lys Gly Pro Leu Arg Met Leu Val
260 265 270

Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
275 280 285

Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
290 295 300

Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu Ser Thr
305 310 315 320

Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe
325 330 335

Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
340 345 350

Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile
355 360 365

Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
370 375 380

Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
385 390 395 400

Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
405 410 415

Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
420 425 430

Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
435 440 445

Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
450 455 460

Phe Tyr Ile
465

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2765 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 249..1649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

TGGGACAGGC AGCTCCGGGG TCCGCGTTT CACATCGGAA ACAAAACAGC GGCTGGTCTG	60
GAAGGAAACCT GAGCTACGAG CGCGGGCGGC AGCGGGGCGG CGGGGAAGCG TATACTAAAT	120
CTGGGAGCCT GCAAGTGACA ACAGCCTTTG CGGTCTTAG ACAGCTTGGC CTGGAGGAGA	180
ACACATGAAA GAAAGAACCT CAAGAGGCTT TGTTTCTGT GAAACAGTAT TTCTATACAG	240
TTGCTCCA ATG ACA GAG TTA CCT GCA CCG TTG TCC TAC TTC CAG AAT GCA	290
Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala	

1	5	10	
CAG ATG TCT GAG GAC AAC CAC CTG AGC AAT ACT GTC CGT AGC CAG CAG AAT Gln Met Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn 15 20 25 30			338
GAC AAT AGA GAA CGG CAG GAG CAC AAC GAC AGA CGG AGC CTT GGC CAC Asp Asn Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His 35 40 45			386
CCT GAG CCA TTA TCT AAT GGA CGA CCC CAG GGT AAC TCC CGG CAG GTG Pro Glu Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val 50 55 60			434
GTG GAG CAA GAT GAG GAA GAT GAG GAG CTG ACA TTG AAA TAT GGC Val Glu Gln Asp Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly 65 70 75			482
GCC AAG CAT GTG ATC ATG CTC TTT GTC CCT GTG ACT CTC TGC ATG GTG Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val 80 85 90			530
GTG GTC GTG GCT ACC ATT AAG TCA GTC AGC TTT TAT ACC CGG AAG GAT Val Val Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp 95 100 105 110			578
GGG CAG CTA ATC TAT ACC CCA TTC ACA GAA GAT ACC GAG ACT GTG GGC Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly 115 120 125			626
CAG AGA GCC CTG CAC TCA ATT CTG AAT GCT GCC ATC ATG ATC AGT GTC Gln Arg Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val 130 135 140			674
ATT GTT GTC ATG ACT ATC CTC CTG GTG TTG CTG TAT AAA TAC AGG TGC Ile Val Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys 145 150 155			722
TAT AAG GTC ATC CAT GCC TGG CTT ATT ATA TCA TCT CTA TTG TTG CTG Tyr Lys Val Ile His Ala Trp Leu Ile Ser Ser Leu Leu Leu Leu 160 165 170			770
TTC TTT TTT TCA TTC ATT TAC TTG GGG GAA GTG TTT AAA ACC TAT AAC Phe Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn 175 180 185 190			818
GTT GCT GTG GAC TAC ATT ACT GTT GCA CTC CTG ATC TGG AAT TTT GGT Val Ala Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly 195 200 205			866
GTG GTG GGA ATG ATT TCC ATT CAC TGG AAA GGT CCA CTT CGA CTC CAG Val Val Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln 210 215 220			914
CAG GCA TAT CTC ATT ATG ATT AGT GCC CTC ATG GCC CTG GTG TTT ATC Gln Ala Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile 225 230 235			962
AAG TAC CTC CCT GAA TGG ACT GCG TGG CTC ATC TTG GCT GTG ATT TCA Lys Tyr Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser 240 245 250			1010

GTA TAT GAT TTA GTG GCT TTG TGT CTG AAA GGT CCA CTT CGT ATG Val Tyr Asp Leu Val Ala Val Leu Cys Leu Lys Gly Pro Leu Arg Met 255	260	265	270	1058
CTG GTT GAA ACA GCT CAG GAG AGA AAT GAA ACG CTT TTT CCA GCT CTC Leu Val Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu 275	280	285		1106
ATT TAC TCC TCA ACA ATG GTG TGG TTG GTG AAT ATG GCA GAA GGA GAC Ile Tyr Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp 290	295	300		1154
CCG GAA GCT CAA AGG AGA GTA TCC AAA AAT TCC AAG CAT AAT GCA GAA Pro Glu Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu 305	310	315		1202
AGC ACA GAA AGG GAG TCA CAA GAC ACT GTT GCA GAG AAT GAT GAT GGC Ser Thr Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly 320	325	330		1250
GGG TTC AGT GAG GAA TGG GAA GCC CAG AGG GAC AGT CAT CTA GGG CCT Gly Phe Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro 335	340	345	350	1298
CAT CGC TCT ACA CCT GAG TCA CGA GCT GCT GTC CAG GAA CTT TCC AGC His Arg Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser 355	360	365		1346
AGT ATC CTC GCT GGT GAA GAC CCA GAG GAA AGG GGA GTA AAA CTT GGA Ser Ile Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly 370	375	380		1394
TTG GGA GAT TTC ATT TTC TAC AGT GTT CTG GTT GGT AAA GCC TCA GCA Leu Gly Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala 385	390	395		1442
ACA GCC AGT GGA GAC TGG AAC ACA ACC ATA GCC TGT TTC GTA GCC ATA Thr Ala Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile 400	405	410		1490
TTA ATT GGT TTG TGC CTT ACA TTA TTA CTC CTT GCC ATT TTC AAG AAA Leu Ile Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys 415	420	425	430	1538
GCA TTG CCA GCT CTT CCA ATC ATC ACC TTT GGG CTT GTT TTC TAC Ala Leu Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr 435	440	445		1586
TTT GCC ACA GAT TAT CTT GTA CAG CCT TTT ATG GAC CAA TTA GCA TTC Phe Ala Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe 450	455	460		1634
CAT CAA TTT TAT ATC TAGCATATTT GCGGTTAGAA TCCCCATGGAT GTTTCTTCTT His Gln Phe Tyr Ile 465				1689
TGACTATAAC CAAATCTGGG GAGGACAAAG GTGATTTCC TGTGTCCACA TCTAACAAAG				1749
TCAAGATTCC CGGCTGGACT TTTGAGCTT CCTTCCAAGT CTTCTGACC ACCTTGCAC				1809
ATTGGACTTT GGAAGGAGGT GCCTATAGAA AACGATTTG AACATACCTC ATCGCAGTGG				1869

ACTGTGTCCC TCGGTGCAGA AACTACCAGA	TTTGAGGGAC GAGGTCAAGG AGATATGATA	1929
GGCCCGGAAG TTGCTGTGCC CCATCAGCG	CTTGACGCGT GGTCACAGGA CGATTTCAC	1989
GACACTGCGA ACTCTCAGGA CTACCGGTTA	CCAAGAGGTT AGGTGAAGTG GTTTAACCA	2049
AACCGAACTC TTCATCTTAA ACTACACGTT	GAAAATCAAC CCAATAATTC TGATTAAC	2109
GAATTCTGAA CTTTCAGGA GGTACTGTGA	GGAAAGAGCAG GCACCAGCAG CAGAATGGGG	2169
ATGGGAGAGG TGGGCAGGGG TTCCAGCTTC	CCTTGTATT TTTGCTGCAG ACTCATCCTT	2229
TTTAAATGAG ACTTGTTC CCCTCTTT	GAGTCAGTC AAATATGTAG ATTGCCTTG	2289
GCAATTCTTC TTCTCAAGCA CTGACACTA	TTACCGTCTG TGATTGCCAT TTCTTCCCAA	2349
GGCCAGCTG AACCTGAGGT	TGCTTTATCC TAAAAGTTT AACCTCAGGT TCCAAATTCA	2409
GTAAATTTG GAAACAGTAC AGTATTTCT	CATCAATTCT CTATCATGTT GAAGTCAAAT	2469
TTGGATTTC CACCAAATTC	TGAATTTGTA GACATACTTG TACGCTACT TGCCCCCAGA	2529
TGCCCTCCT GTCCCTCATTC	TTCTCTCCCA CACAAGCAGT CTTTTCTAC AGCCAGTAAG	2589
GCAGCTCTGT CRTGGTAGCA	GATGGTCCA TTATTCAGG GTCTTACTCT TTGTATGATG	2649
AAAAGAATGT GTTATGAATC	GGTGCTGTCA GCCCTGCTGT CAGACCTTCT TCCACAGCAA	2709
ATGAGATGTA TGCCCAAAGC	GGTAGAATTA AAGAAGAGTA AAATGGCTGT TGAAGC	2765

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 467 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met			
1	5	10	15

Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn Asp Asn		
20	25	30

Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His Pro Glu		
35	40	45

Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu		
50	55	60

Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys			
65	70	75	80

His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val		
85	90	95

Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln		
100	105	110

Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
115 120 125

Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
130 135 140

Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
145 150 155 160

Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu Phe Phe
165 170 175

Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
180 185 190

Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val
195 200 205

Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
210 215 220

Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
225 230 235 240

Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
245 250 255

Asp Leu Val Ala Val Leu Cys Leu Lys Gly Pro Leu Arg Met Leu Val
260 265 270

Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
275 280 285

Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
290 295 300

Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu Ser Thr
305 310 315 320

Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe
325 330 335

Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
340 345 350

Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile
355 360 365

Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
370 375 380

Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
385 390 395 400

Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
405 410 415

Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
420 425 430

Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
435 440 445

Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
450 455 460

Phe Tyr Ile
465

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2765 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 249..1649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

TGGGACAGGC AGCTCCGGGG TCCGCGGTTT CACATCGGAA ACAAAACAGC GGCTGGTCTG	60
GAAGGAAACCT GAGCTACGAG CGCGCGCGC AGCGGGGCGG CGGGGAAGCG TATACTTAAT	120
CTGGGAGCCT GCAAGTGTACA ACAGCCTTTG CGGTCTTAG ACAGCTTGCC CTGGAGGAGA	180
ACACATGAAA GAAAGAACCT CAAGAGGCTT TGTTTCTGT GAAACAGTAT TTCTATACAG	240
TTGGTCCA ATG ACA GAG TTA CCT GCA CCG TTG TCC TAC TTC CAG AAT GCA	290
Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala	
1 5 10	
CAG ATG TCT GAG GAC AAC CAC CTG AGC AAT ACT GTC CGT AGC CAG AAT	338
Gln Met Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn	
15 20 25 30	
GAC AAT AGA GAA CGG CAG GAG CAC AAC GAC AGA CGG AGC CTT GGC CAC	386
Asp Asn Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His	
35 40 45	
CCT GAG CCA TTA TCT AAT GGA CGA CCC CAG GGT AAC TCC CGG CAG GTG	434
Pro Glu Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val	
50 55 60	
GTG GAG CAA GAT GAG GAA GAA GAT GAG GAG CTG ACA TTG AAA TAT GGC	482
Val Glu Gln Asp Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly	
65 70 75	
GCC AAG CAT GTG ATC ATG CTC TTT GTC CCT GTG ACT CTC TGC ATG GTG	530
Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val	
80 85 90	
GTG GTC GTG GCT ACC ATT AAG TCA GTC AGC TTT TAT ACC CGG AAG GAT	578
Val Val Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp	
95 100 105 110	
GGG CAG CTA ATC TAT ACC CCA TTC ACA GAA GAT ACC GAG ACT GTG GGC	626

Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly	115	120	125	
CAG AGA GCC CTG CAC TCA ATT CTG AAT GCT GCC ATC ATG ATC AGT GTC				674
Gln Arg Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val	130	135	140	
ATT GTT GTC ATG ACT ATC CTC CTG GTG GTT CTG TAT AAA TAC AGG TGC				722
Ile Val Val Met Thr Ile Leu Val Val Leu Tyr Lys Tyr Arg Cys	145	150	155	
TAT AAG GTC ATC CAT GCC TGG CTT ATT ATA TCA TCT CTA TTG TTG CTG				770
Tyr Lys Val Ile His Ala Trp Leu Ile Ser Ser Leu Leu Leu Leu	160	165	170	
TTC TTT TTT TCA TTC ATT TAC TTG GGG GAA GTG TTT AAA ACC TAT AAC				818
Phe Phe Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn	175	180	185	
GTT GCT GTG GAC TAC ATT ACT GTT GCA CTC CTG ATC TGG AAT TTT GGT				866
Val Ala Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly	195	200	205	
GTG GTG GGA ATG ATT TCC ATT CAC TGG AAA GGT CCA CTT CGA CTC CAG				914
Val Val Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln	210	215	220	
CAG GCA TAT CTC ATT ATG ATT AGT GCC CTC ATG GCC CTG GTG TTT ATC				962
Gln Ala Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile	225	230	235	
AAG TAC CTC CCT GAA TGG ACT GCG TGG CTC ATC TTG GCT GTG ATT TCA				1010
Lys Tyr Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser	240	245	250	
GTA TAT GAT TTA GTG GCT GTT TTG TGT CCG AAA GGT CCA CTT CAT ATG				1058
Val Tyr Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu His Met	255	260	265	
CTG GTT GAA ACA GCT CAG GAG AGA AAT GAA ACG CTT TTT CCA GCT CTC				1106
Leu Val Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu	275	280	285	
ATT TAC TCC TCA ACA ATG GTG TGG TTG GTG AAT ATG GCA GAA GGA GAC				1154
Ile Tyr Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp	290	295	300	
CCG GAA GCT CAA AGG AGA GTA TCC AAA AAT TCC AAG CAT AAT GCA GAA				1202
Pro Glu Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu	305	310	315	
AGC ACA GAA AGG GAG TCA CAA GAC ACT GTT GCA GAG AAT GAT GAT GGC				1250
Ser Thr Glu Arg Glu Ser Glu Asp Thr Val Ala Glu Asn Asp Asp Gly	320	325	330	
GGG TTC AGT GAG GAA TGG GAA GCC CAG AGG GAC AGT CAT CTA GGG CCT				1298
Gly Phe Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro	335	340	345	
CAT CGC TCT ACA CCT GAG TCA CGA GCT GCT GTC CAG GAA CTT TCC AGC				1346
His Arg Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser	355	360	365	

AGT ATC CTC GCT GGT GAA GAC CCA GAG GAA AGG GGA GTA AAA CTT GGA Ser Ile Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly 370 375 380	1394
TTG GGA GAT TTC ATT TTC TAC AGT GTT CTG GTT GGT AAA GCC TCA GCA Leu Gly Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala 385 390 395	1442
ACA GCC AGT GGA GAC TGG AAC ACA ACC ATA GCC TGT TTC GTA GCC ATA Thr Ala Ser Gly Asp Trp Asn Thr Ile Ala Cys Phe Val Ala Ile 400 405 410	1490
TTA ATT GGT TTG TGC CTT ACA TTA TTA CTC CTT GCC ATT TTC AAG AAA Leu Ile Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys 415 420 425 430	1538
GCA TTG CCA GCT CTT CCA ATC TCC ATC ACC TTT GGG CTT GTT TTC TAC Ala Leu Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr 435 440 445	1586
TTT GCC ACA GAT TAT CTT GTA CAG CCT TTT ATG GAC CAA TTA GCA TTC Phe Ala Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe 450 455 460	1634
CAT CAA TTT TAT ATC TAGCATATTG CGCGTTAGAA TCCCCATGGAT GTTTCTTCTT His Gln Phe Tyr Ile 465	1689
TGACTATAAC CAAATCTGGG GAGGACAAAG GTGATTTCC TGTGTCCACA TCTAACAAAG	1749
TCAAGATTCC CGGCTGGACT TTTGCAGCTT CCTTCCAAGT CTTCTGACC ACCTTGCACT	1809
ATGGACTTT GGAAGGAGGT GCCTATAGAA AACGATTTG AACATACTTC ATCGCAGTGG	1869
ACTGTGTCCC TCGGTGCAGA AACTACCAGA TTTGAGGGAC GAGGTCAAGG AGATATGATA	1929
GGCCCGGAAG TTGCTGTGCC CCATCAGCAC CTTGACGCGT GGTCACAGGA CGATTCTCACT	1989
GACACTCGCA ACTCTCAGGA CTACCGGTTA CCAAGAGGTT AGGTGAAGTG GTTAAACCA	2049
AACGGAACCTT TTCTATCTAA ACTACACGTT GAAAATCAAC CCAATAATTG TGTTATTAACT	2109
GAATTCTGAA CTTTCAGGA GGTACTCTGA GGAAGAGCG GCACCCAGCG CAGAATGGGG	2169
ATGGAGAGG TGGGCAGGGG TTCCAGCTTC CCTTTGATTG TTTGCTGCAG ACTCATCCTT	2229
TTTAAATGAG ACTTGTTC CCCTCTCTT GAGTCAGTC AAATATGTAG ATTGCCTTTC	2289
GCAATTCTTC TTCTCAAGCA CTGACACTCA TTACCGCTCTG TGATTGCCAT TTCTTCCCAA	2349
GGCCAGCTCTG AACCTGAGGT TGCTTTATCC TAAAAGTTT AACCTCAGGT TCCAAATTCA	2409
GTAAATTG GAAACAGTAC AGCTATTCT CATCAATTCT CTATCATGTT GAAGTCAGT	2469
TTGGATTTTC CACCAAATTC TGAATTGTA GACATACTTG TAGCCTCACT TGCCCCAGA	2529
TGCCTCCCTCT GTCCTCATTC TTCTCTCCCA CACAAGCAGT CTTTTCTAC AGCCAGTAA	2589
GCAGCTCTGT CRTGGTAGCA GATGGTCCCA TTATTCTAGG GTCTTACTCT TTGTATGATG	2649
AAAAGAATGT GTTATGAATC GGTGCTGTCA GCCCTGCTGT CAGACCTTCT TCCACAGCAA	2709

ATGAGATGTA TGCCCAAAGC GGTAGAATTAA AAGAAGAGTA AAATGGCTGT TGAAGC

2765

(2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 467 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met
1 5 10 15

Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn Asp Asn
20 25 30

Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His Pro Glu
35 40 45

Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu
50 55 60

Gln Asp Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
65 70 75 80

His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
85 90 95

Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
100 105 110

Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
115 120 125

Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
130 135 140

Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
145 150 155 160

Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Phe Phe
165 170 175

Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
180 185 190

Val Asp Tyr Ile Thr Val Ala Leu Ile Trp Asn Phe Gly Val Val
195 200 205

Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
210 215 220

Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
225 230 235 240

Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
245 250 255

Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu His Met Leu Val

260	265	270
Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr		
275	280	285
Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu		
290	295	300
Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu Ser Thr		
305	310	315
Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe		
325	330	335
Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg		
340	345	350
Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile		
355	360	365
Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly		
370	375	380
Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala		
385	390	395
Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile		
405	410	415
Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu		
420	425	430
Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala		
435	440	445
Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln		
450	455	460
Phe Tyr Ile		
465		